



FIGURE 1

SEQ ID NO:51	GAC	GGA	ATT	AAT	TTC	GCA	ACA	GGG	AAT	TTA	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG
SEQ ID NO:52	D	G	I	N	F	A	T	G	N	L	P	G	C	S	F	S	I	F	L	L

SEQ ID NO:51	GCT TTG TTC TCA TGC TTG CTT ACA CCC ACA GCC GGG CTG GAG TAC CGT AAT GCC TCC GGA
SEQ ID NO:52	A L F S C L L T P T A G
	L E Y R N A S G
	SEQ ID NO:138 (page 5)

SEQ ID NO:51	CTC TAC ATG GTA ACT AAC GAC TGC AGT AAC GGT AGT ATC GTG TAT GAG GCC GGG GAT ATT
SEQ ID NO:52	L Y M V T N D C S N G S I V Y E A G D I
SEQ ID NO:138	SEQ ID NO:155 (Page 6) 217

SEQ ID NO:51	ATC CTC CAC TTA CCT GGC TGT GTC CCC TGC GTA CGC TCT GGC AAT ACA TCA AGA TGG
SEQ ID NO:52	I L H L P G C V P C V R S G N T S R C W
SEQ ID NO:155	T
	SEQ ID NO:174 (page 6)

SEQ ID NO:51	ATC CCT GTG AGC CCY	ACC GTC	GCC GTG AAG TCG CCC TGC GCC ACC TCT CTC CGC	
SEQ ID NO:52	I P V S P T V A	V K S P C	A T A S	L R
SEQ ID NO:174	G			SEQ ID NO:190 (page
			252	

SEQ ID NO:51 ACG CAC GTG GAT ATG ATG GTG GGR
SEQ ID NO:52 T H V D M M V G A A T L C S A L Y V G D
A wobble, no effect on translation

SEQ ID NO:51 CTT TGT GGA GCG CTA TTT CTT GTT GGG CAG GGG TTC TCA TGG AGA CAT CGC CAG CAT TGG wobble, no effect on translation
SEQ ID NO:52 L C G A L F L V G Q G F S W R H R Q H W

SEQ	ID NO:51	ACT	GTC	CAG	GAC	TGC	AAC	TGT	TCC	ATC
SEQ	ID NO:52	T	V	Q	D	C	N	C	S	I



Figure 2 (page 1 of 2)
E1 nucleic acid

51 HOTTA '046	GACGGAAATTAA ATTTCGCAAC AGGGAATTAA CCTGGTTGCT CTTTCTCTAT CTTCCATTCTG GCTTTGTTCTT CATGCTTGCT TACACCCACA GCCGGGCTGG AGTACCGTAA TGCTCCGGAA CTCT CATGCTTGCT TACACCCACA GCGGGGTGG AGTATCGTAA TGCTCCGGAA
51 HOTTA '046	CTCTACATGG TAACTAACGA CTGCAGTAAC GGTAGTATCG TGTATGAGGC CGGGGATATT CTCTACATAG TAACCAACGA CTGCAGTAAC AGCAGTATCG TGTATGAGGC CCAAGGATATT
51 HOTTA '046	ATCCTCCACT TACCTGGCTG TGTCCCCCTGC GTACGCTCTG GCAATAACATC AAGATGCTGG ATCCTCCACA TGCCTGGCTG TGAACCCCCCTGC GTACGCTCTG GCAACACATC AAGGTGCTGG
51 HOTTA '046	ATCCCCTGTGA GCCCYACCGT CGCCGTGAAG TCGCCCTGGC CGCCCACCGC CTCTCTCCGC ACCCTGTAA GCTCTACTGT CGCTGTGGGT CGCGCTGGCG CTGCTACCGC CTCTCTCCGC
51 HOTTA '046	ACGCACCGTGG ATATGATGGT GGGRGGGGCC ACCCTATGCT CAGCTCTCTA CGTAGGGAGAC ACCATGTGG ATATGATGGT GGAAGGGCC ACCCTTGTCT CAGCTCTCTA CGTAGGGAGAC
51 HOTTA '046	CTTTGTGGAG CGCTTATTCT TGTYGGCAG GGGTTCTCAT GGAGACATCG CCAGCATGG CTTGTGGAG CGCTTATTCT TGTGGCAG GGGTTCTCAT GGAGACATCG CCAGCATGG
51 HOTTA '046	ACTGTCCAGG ACTGCAACTG TTCCATC ACTGTCCAGG ATGCAACTG TTGGATCTAC CCTGGGCACC TAACAGGCCA TCGTATG

Figure 2 (page 2 of 2)
E1 protein



Hotta '046	52	DGINFATGNL PGCSFSIPLL ALFSCLE TPT ISCLLTPT	AGLEYRNASC LYMVTNDCSN GSIVYEAGD AGLEYRNASC LYIVTNDCSN SSIIVYEAQDI
Hotta '046	52	ILHLPGCCVPC VRSGNTSRCW IPVSPTVAVK ILHM P GCDPC VRSGNTSRCW TPVSS T VAVG	SPCAATTASLR THYDMMVGAA TLCSALYVGD RAGAATTASLR THYDMMVGAA TLCSALYVGD
Hotta '046	52	LCGALFLVGQ GFSWRHRQHW TVQDCNCSSI LCGALFLVGQ GFSWRHRQHW TVQDCNCSSI PGHLTGHRM	